

RAW SEQUENCE LISTING

DATE: 06/29/2001

PATENT APPLICATION: US/09/424,840A

TIME: 13:48:08

Input Set : A:\5649049.app

Output Set: N:\CRF3\06292001\I424840A.raw

3 <110> APPLICANT: BERCHTOLD, Peter
 4 ESCHER, Robert F.A.
 6 <120> TITLE OF INVENTION: Anti-GPIIB/IIIA Recombinant Antibodies
 8 <130> FILE REFERENCE: 100564-09049
 10 <140> CURRENT APPLICATION NUMBER: US 09/424,840A
 11 <141> CURRENT FILING DATE: 1999-12-03
 13 <150> PRIOR APPLICATION NUMBER: DE 19723904.8
 14 <151> PRIOR FILING DATE: 1997-06-06
 16 <150> PRIOR APPLICATION NUMBER: DE 19755227.7
 17 <151> PRIOR FILING DATE: 1997-12-12
 19 <150> PRIOR APPLICATION NUMBER: DE 19820663.1
 20 <151> PRIOR FILING DATE: 1998-05-08
 22 <160> NUMBER OF SEQ ID NOS: 127
 24 <170> SOFTWARE: PatentIn Ver. 2.1

26 <210> SEQ ID NO: 1
 27 <211> LENGTH: 357
 28 <212> TYPE: DNA
 29 <213> ORGANISM: Homo sapiens
 31 <220> FEATURE:
 32 <221> NAME/KEY: CDS
 33 <222> LOCATION: (1)..(357)
 35 <400> SEQUENCE: 1

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37	Gln	Val	Lys	Leu	Leu	Glu	Ser	Gly	Pro	Gly	Leu	Val	Lys	Pro	Ser	Glu	
38	1				5					10					15		
40	acc	ctg	tcc	ctc	aac	tgc	act	gtc	tct	ggg	cgc	tcc	atc	agt	ggt	tac	96
41	Thr	Leu	Ser	Leu	Asn	Cys	Thr	Val	Ser	Gly	Arg	Ser	Ile	Ser	Gly	Tyr	
42				20					25				30				
44	tct	tgg	aga	tgg	atc	cgg	cag	tct	cca	ggg	aag	gga	cta	gag	tgg	att	144
45	Ser	Trp	Arg	Trp	Ile	Arg	Gln	Ser	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Ile	
46		35					40					45					
48	ggg	gat	atc	tct	tat	agt	ggg	agt	acc	aag	tac	aaa	ccc	tcc	ctc	agg	192
49	Gly	Asp	Ile	Ser	Tyr	Ser	Gly	Ser	Thr	Lys	Tyr	Lys	Pro	Ser	Leu	Arg	
50		50				55					60						
52	agt	cga	gtc	acc	ctg	tca	gta	gac	acg	tcc	aag	aac	cag	ttc	tcc	ctg	240
53	Ser	Arg	Val	Thr	Leu	Ser	Val	Asp	Thr	Ser	Lys	Asn	Gln	Phe	Ser	Leu	
54	65				70				75						80		
56	aag	ctg	aat	tcg	gtg	acc	gct	gcg	gac	acg	gcc	gtc	tat	tac	tgt	gcg	288
57	Lys	Leu	Asn	Ser	Val	Thr	Ala	Ala	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	
58			85					90				95					
60	cga	gtc	ttg	ccc	ttt	gac	ccg	atc	tcg	atg	gac	gtc	tgg	ggc	aaa	ggg	336
61	Arg	Val	Leu	Pro	Phe	Asp	Pro	Ile	Ser	Met	Asp	Val	Trp	Gly	Lys	Gly	
62			100					105					110				
64	acc	acg	gtc	acc	gtc	tcc	tca										357
65	Thr	Thr	Val	Thr	Val	Ser	Ser										
66			115														
69	<210>	SEQ ID NO:	2														

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70 <211> LENGTH: 119
71 <212> TYPE: PRT
72 <213> ORGANISM: Homo sapiens
74 <400> SEQUENCE: 2
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79           20           25           30
81 Ser Trp Arg Trp Ile Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Ile
82           35           40           45
84 Gly Asp Ile Ser Tyr Ser Gly Ser Thr Lys Tyr Lys Pro Ser Leu Arg
85           50           55           60
87 Ser Arg Val Thr Leu Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
88   65           70           75           80
90 Lys Leu Asn Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
91           85           90           95
93 Arg Val Leu Pro Phe Asp Pro Ile Ser Met Asp Val Trp Gly Lys Gly
94           100          105          110
96 Thr Thr Val Thr Val Ser Ser
97           115
101 <210> SEQ ID NO: 3
102 <211> LENGTH: 333
103 <212> TYPE: DNA
104 <213> ORGANISM: Homo sapiens
106 <220> FEATURE:
107 <221> NAME/KEY: CDS
108 <222> LOCATION: (1)..(333)
110 <400> SEQUENCE: 3
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113   1           5           10           15
115 acc atc tct tgt tct ggg agc agc tcc aac atc aga agt aat cct gtt 96
116 Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Arg Ser Asn Pro Val
117           20           25           30
119 agc tgg tat cac cag gtc cca ggc acg gcc ccc aaa ctc ctc atc ttt 144
120 Ser Trp Tyr His Gln Val Pro Gly Thr Ala Pro Lys Leu Leu Ile Phe
121           35           40           45
123 ggt agt cat cag cgg ccc tca ggg gtc cct gac cga ttc tct ggc tcc 192
124 Gly Ser His Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
125           50           55           60
127 aag tcg ggc acc tcc gcc tcc ctg gcc atc cgt ggg ctc caa tct ggg 240
128 Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Arg Gly Leu Gln Ser Gly
129   65           70           75           80
131 gat gct ggt gac tat tac tgt gca aca tgg gat gac ggc ctc aat ggt 288
132 Asp Ala Gly Asp Tyr Tyr Cys Ala Thr Trp Asp Asp Gly Leu Asn Gly
133           85           90           95
135 ccg gtg ttc ggc gga ggg acc aag ctg acc gtc cta agt cag ccc 333
136 Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ser Gln Pro
137           100          105          110

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140 <210> SEQ ID NO: 4
141 <211> LENGTH: 111
142 <212> TYPE: PRT
143 <213> ORGANISM: Homo sapiens
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149 Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Arg Ser Asn Pro Val
150   20          25          30
152 Ser Trp Tyr His Gln Val Pro Gly Thr Ala Pro Lys Leu Leu Ile Phe
153   35          40          45
155 Gly Ser His Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
156   50          55          60
158 Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Arg Gly Leu Gln Ser Gly
159   65          70          75          80
161 Asp Ala Gly Asp Tyr Tyr Cys Ala Thr Trp Asp Asp Gly Leu Asn Gly
162   85          90          95
164 Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ser Gln Pro
165   100         105         110
169 <210> SEQ ID NO: 5
170 <211> LENGTH: 369
171 <212> TYPE: DNA
172 <213> ORGANISM: Homo sapiens
174 <220> FEATURE:
175 <221> NAME/KEY: CDS
176 <222> LOCATION: (1)..(369)
178 <400> SEQUENCE: 5
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180 Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
181   1          5          10          15
183 tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt agc tat      96
184 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
185   20          25          30
187 gct atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg      144
188 Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
189   35          40          45
191 gca gtt ata tca tat gat gga agc aat aaa tac tac gca gac tcc gtg      192
192 Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
193   50          55          60
195 aag ggc cga ttc gcc atc tcc aga gac aat tcc aag aac acg ctg tat      240
196 Lys Gly Arg Phe Ala Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
197   65          70          75          80
199 ctg caa atg aac agc ctg aga gct gag gac acg gct gtg tat tac tgt      288
200 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
201   85          90          95
203 gcg aga gcg ctg ggg agc tgg ggg ggt tgg gac cac tac atg gac gtc      336
204 Ala Arg Ala Leu Gly Ser Trp Gly Gly Trp Asp His Tyr Met Asp Val
205   100         105         110
207 tgg ggc aaa ggg acc acg gtc acc gtc tcc tca      369

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215 <213> ORGANISM: Homo sapiens
217 <400> SEQUENCE: 6
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219 1      5      10      15
221 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
222      20      25      30
224 Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
225      35      40      45
227 Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
228      50      55      60
230 Lys Gly Arg Phe Ala Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
231 65      70      75      80
233 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
234      85      90      95
236 Ala Arg Ala Leu Gly Ser Trp Gly Gly Trp Asp His Tyr Met Asp Val
237      100     105     110
239 Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
240      115     120
244 <210> SEQ ID NO: 7
245 <211> LENGTH: 333
246 <212> TYPE: DNA
247 <213> ORGANISM: Homo sapiens
249 <220> FEATURE:
250 <221> NAME/KEY: CDS
251 <222> LOCATION: (1)..(333)
253 <400> SEQUENCE: 7
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258 acc atc tct tgt tct gga agc agc tcc aac atc gga agt aat act gta 96
259 Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn Thr Val
260      20      25      30
262 aac tgg tac cag cag ctc cca gga acg gcc ccc aaa ctc ctc atc tat 144
263 Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr
264      35      40      45
266 agt aat aat cag cgg ccc tca ggg gtc cct gac cga ttc tct ggc tcc 192
267 Ser Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
268      50      55      60
270 aag tct ggc acc tca gcc tcc ctg gcc atc agt ggg ctc cag tct gag 240
271 Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln Ser Glu
272 65      70      75      80
274 gat gag gct gat tat tac tgt gca gca tgg gat gac agc ctg aat ggt 288
275 Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu Asn Gly
276      85      90      95

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278 tgg gtg ttc ggc gga ggg acc aag ctg acc gtc cta ggt cag ccc 333
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284 <211> LENGTH: 111
285 <212> TYPE: PRT
286 <213> ORGANISM: Homo sapiens
288 <400> SEQUENCE: 8
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290      1      5      10      15
292 Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn Thr Val
293      20      25      30
295 Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr
296      35      40      45
298 Ser Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
299      50      55      60
301 Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln Ser Glu
302      65      70      75      80
304 Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu Asn Gly
305      85      90      95
307 Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro
308      100      105      110
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313 <211> LENGTH: 369
314 <212> TYPE: DNA
315 <213> ORGANISM: Homo sapiens
317 <220> FEATURE:
318 <221> NAME/KEY: CDS
319 <222> LOCATION: (1)..(369)
321 <400> SEQUENCE: 9
322 'cag gtg aaa ctg ctc gag tct ggg gga ggc ttg gtt cac ccc ggg ggg 48
323 Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Leu Val His Pro Gly Gly
324      1      5      10      15
326 tcc ctg aga ctc tct tgt gca gcc tct gga ttt acg ttt gac aac ttt 96
327 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asn Phe
328      20      25      30
330 gcc atg agc tgg gtc cgc cag gct cca ggg aag ggg ctg gag tgg gtc 144
331 Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
332      35      40      45
334 tca ggc att agt ggt ggt ggt ctt ttg aca cac tac gca gac tcc gtg 192
335 Ser Gly Ile Ser Gly Gly Gly Leu Leu Thr His Tyr Ala Asp Ser Val
336      50      55      60
338 aag ggc cgg ttc acc atc tcc aga aac aat tcc agg aac act gta tac 240
339 Lys Gly Arg Phe Thr Ile Ser Arg Asn Asn Ser Arg Asn Thr Val Tyr
340      65      70      75      80
342 cta caa atg aac agc ctg aga gcc gaa gac acg gcc gtg tat tat tgt 288
343 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
344      85      90      95
346 gtg aga gat ctg ggc tat aga gta ctt tcg act ttt act ttt gat atc 336

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VERIFICATION SUMMARY

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